

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Hillman, Jennifer
Corley, Neil C.
Shah, Purvi

(ii) TITLE OF THE INVENTION: NEW ANEXIN BINDING PROTEIN

(iii) NUMBER OF SEQUENCES: 3

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
(B) STREET: 3174 Porter Drive
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: Herewith
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Billings, Lucy J.
(B) REGISTRATION NUMBER: 36,749
(C) REFERENCE/DOCKET NUMBER: PF-0354-2 DIV

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-855-0555
(B) TELEFAX: 650-845-4166
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 290 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: PROSNON01
(B) CLONE: 2272281

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Lys Arg Asn Ser Pro Gln Lys Ile Lys Lys Arg Lys Asp Arg Arg
 1 5 10 15
 Ala Lys Lys Gln Ser Phe Asp Asp Asn Asp Ser Glu Glu Leu Glu Asp
 20 25 30
 Lys Asp Ser Lys Ser Lys Lys Thr Ala Lys Pro Lys Val Glu Met Tyr
 35 40 45
 Ser Gly Ser Asp Asp Asp Asp Asp Phe Asn Lys Leu Pro Lys Lys Ala
 50 55 60
 Lys Gly Lys Ala Gln Lys Ser Asn Lys Lys Trp Asp Gly Ser Glu Glu
 65 70 75 80
 Asp Glu Asp Asn Ser Lys Lys Ile Lys Glu Arg Ser Arg Ile Asn Ser
 85 90 95
 Ser Gly Glu Ser Gly Asp Glu Ser Asp Glu Phe Leu Gln Ser Arg Lys
 100 105 110
 Gly Gln Lys Lys Asn Gln Lys Asn Lys Pro Gly Pro Asn Ile Glu Ser
 115 120 125
 Gly Asn Glu Asp Asp Asp Ala Ser Phe Lys Ile Lys Thr Val Ala Gln
 130 135 140
 Lys Lys Ala Glu Lys Lys Glu Arg Glu Arg Lys Lys Arg Asp Glu Glu
 145 150 155 160
 Lys Ala Lys Leu Arg Lys Leu Lys Glu Lys Glu Glu Leu Glu Thr Gly
 165 170 175
 Lys Lys Asp Gln Ser Lys Gln Lys Glu Ser Gln Arg Lys Phe Glu Glu
 180 185 190
 Glu Thr Val Lys Ser Lys Val Thr Val Asp Thr Gly Val Ile Pro Ala
 195 200 205
 Ser Glu Glu Lys Ala Glu Thr Pro Thr Ala Ala Glu Asp Asp Asn Glu
 210 215 220
 Gly Asp Lys Lys Lys Asp Lys Lys Lys Lys Gly Glu Lys Glu
 225 230 235 240
 Glu Lys Glu Lys Lys Lys Gly Pro Ser Lys Ala Thr Val Lys
 245 250 255
 Ala Met Gln Glu Ala Leu Ala Lys Leu Lys Glu Glu Glu Arg Gln
 260 265 270
 Lys Arg Glu Glu Glu Glu Arg Ile Lys Arg Leu Glu Glu Leu Glu Ser
 275 280 285
 Lys Pro
 290

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1434 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSNON01
- (B) CLONE: 2272281

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CTGTTCCAGT	GCGCGGGTCT	GTGGAGAGCC	GGGTGCGAGC	GGCGGCAGCA	CGAGGGAAA	60
AGAGCTGAGC	GGAGACAAA	GTCAGCCGGG	AGACAGTGGG	TCTGTGAGAG	ACCGAATAGA	120
GGGGCTGGGG	CCACCGAGCGC	CATTGACAAG	CAATGGGGAA	GAAACAGAAA	AACAAGAGCG	180
AAGACAGCAC	CAAGGATGAC	ATTGATCTTG	ATGCCTTGGC	TGCAGAAATA	GAAGGAGCTG	240
GTGCTGCCAA	AGAACAGGAG	CCTCAAAAGT	CAAAGGGAA	AAAGAAAAAA	GAGAAAAAAA	300
AGCAGGACTT	TGATGAAGAT	GATATCCTGA	AAGAACTGGA	AGAATTGTCT	TTGGAAGCTC	360
AAGGCATCAA	AGCTGACAGA	GAAACTGTTG	CAGTGAAGCC	AACAGAAAAAC	AATGAAGAGG	420
AATTCACCTC	AAAAGATAAA	AAAAAGAAAG	GACAGAAGGG	CAAAAAAACAA	GAGTTTTGAT	480

GATAATGATA	GCGAAGAAATT	GGAAGATAAA	GATTCAAAAT	CAAAAAAGAC	TGCAAAACCG	540
AAAGTGAAA	TGTACTCTGG	GAGTGTGAT	GATGATGATT	TTAACAAACT	TCCTAAAAAA	600
GCTAAAGGGA	AAGCTAAAAA	ATCAAATAAG	AAGTGGGATG	GGTCAGAGGA	GGATGAGGAT	660
AACAGTAAAA	AAATTAAAGA	GCGTTCAAGA	ATAAATTCTT	CTGGTAAAG	TGGTGATGAA	720
TCAGATGAAT	TTTTGCAATC	TAGAAAAGGA	CAGAAAAAAA	ATCAGAAAAA	CAAGCCAGGT	780
CCTAACATAG	AAAGTGGGAA	TGAAGATGAT	GACGCCCTCT	TCAAAATTAA	GACAGTGGCC	840
CAAAGAAGG	CAGAAAAGAA	GGAGCGCGAG	AGAAAAAAAGC	GAGATGAAGA	AAAAGCGAAA	900
CTGCGGAAGC	TGAAAGAAAA	AGAAGAGTTA	GAAACAGGTA	AAAAGGATCA	GAGTAAACAA	960
AAGGAATCTC	AAAGGAAATT	TGAAGAAGAA	ACTGTAAAAT	CCAAAGTGC	TGTTGATACT	1020
GGAGTAATTG	CTGCTCTGA	AGAGAAAGCA	GAGACTCCCC	CAGCTGCAGA	AGATGACAAT	1080
GAAGGAGACA	AAAAGAAGAA	AGATAAGAAG	AAAAAGAAAG	GAGAAAAGGA	AGAAAAAGAG	1140
AAAGAGAAGA	AAAAAGGACC	TAGCAAAGCC	ACTGTTAAAG	CTATGCAAGA	AGCTCTGGCT	1200
AAGCTTAAAG	AGGAAGAAGA	AAGACAGAAG	AGAGAAGAGG	AAGAACGTAT	AAAACGGCTT	1260
GAAGAATTAG	AAAGCAAGCC	GTAAGCACAA	GGAACCGTT	GGAACCCAGA	CCAAAAGAGC	1320
AAGGGCACAG	GCAAGACACC	AAACCAAGGG	GCGGCCCG	AATTATGTA	CCTCTTCGCA	1380
CCGGGACTTC	CTTCCGGGGC	CGTTCTGCA	AGCGGAACCA	ATTTTCCCTA	AAGG	1434

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 234 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
 - (B) CLONE: 1514949

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gly	Gln	Lys	Gly	Lys	Lys	Thr	Ser	Phe	Asp	Glu	Asn	Asp	Ser	Glu	Glu	
1				5				10					15			
Leu	Glu	Asp	Lys	Asp	Ser	Lys	Ser	Lys	Lys	Pro	Ala	Arg	Pro	Asn	Ser	
						20			25				30			
Glu	Val	Leu	Leu	Ser	Gly	Ser	Glu	Asp	Ala	Asp	Asp	Pro	Asn	Lys	Leu	
					35		40				45					
Ser	Lys	Lys	Gly	Lys	Lys	Ala	Gln	Lys	Ser	Thr	Lys	Lys	Arg	Asp	Gly	
						50		55			60					
Ser	Glu	Glu	Asp	Glu	Asp	Asn	Ser	Lys	Arg	Ser	Lys	Glu	Arg	Ser	Arg	
						65		70		75			80			
Val	Asn	Ser	Ser	Gly	Glu	Ser	Gly	Gly	Glu	Ser	Asp	Glu	Phe	Leu	Gln	
					85				90				95			
Ser	Arg	Lys	Gly	Gln	Lys	Lys	Asn	Gln	Lys	Asn	Lys	Ser	Val	Pro	Thr	
					100				105				110			
Ile	Asp	Ser	Gly	Asn	Glu	Asp	Asp	Asp	Ser	Ser	Phe	Lys	Ile	Lys	Thr	
					115			120				125				
Val	Ala	Gln	Lys	Lys	Ala	Glu	Lys	Lys	Glu	Arg	Glu	Arg	Lys	Lys	Arg	
					130		135				140					
Glu	Glu	Glu	Lys	Ala	Lys	Leu	Arg	Lys	Val	Lys	Glu	Lys	Glu	Glu	Leu	
						145		150			155			160		
Glu	Lys	Gly	Arg	Lys	Glu	Gln	Ser	Lys	Gln	Arg	Glu	Pro	Gln	Lys	Arg	
						165			170				175			
Pro	Asp	Glu	Glu	Val	Leu	Val	Leu	Arg	Gly	Thr	Pro	Asp	Ala	Gly	Ala	
						180			185			190				
Ala	Ser	Glu	Glu	Lys	Gly	Asp	Ile	Ala	Ala	Thr	Leu	Glu	Asp	Asp	Asn	
						195			200			205				
Glu	Gly	Asp	Lys	Lys	Lys	Lys	Asp	Lys	Lys	Lys	Lys	Lys	Thr	Glu	Lys	
						210		215				220				
Asp	Asp	Lys	Glu	Lys	Glu	Lys	Lys	Lys	Gly							
						225		230								